IN THE CLAIMS:

Applicants, pursuant to 37 C.F.R. § 1.121, submit the following amendments to the claims:

1. (Currently amended) A method for predicting the responsiveness of a subject, with a breast tissue cell proliferative disorder, ~~of the breast tissues~~ to a therapy involving treatment with ~~comprising~~ one or more drugs that ~~which~~ target the estrogen receptor pathway or that are involved in estrogen metabolism, production, or secretion, said method comprising analysing the methylation status of at least one CpG dinucleotide ~~pattern~~ of at least one ~~one or more~~ target nucleic acids ~~comprising genes taken~~ selected from the gene group consisting of STMN1, SFN, S100A2, TGFBR2, TP53, PTGS2, FGFR1, SYK, PITX2, GRIN2D, PSA, CGA, CYP2D6, MSMB, COX7A2L, VTN, PRKCD, ONECUT2, WBP11, CYP2D6, DAG1, ERBB2, S100A2, TFF1, TP53, TMEFF2, ESR1, SYK, RASSF1, PITX2, PSAT1, CGA, ~~and~~ PCAF, and the ~~and/or their~~ regulatory regions thereof by contacting the at least one ~~at least one of said~~ target nucleic acids in a biological sample, obtained from said subject prior to or during the treatment, with one or more agents suitable to ~~that~~ convert cytosine bases that are unmethylated at the 5'-position thereof to a base that is detectably dissimilar to cytosine in terms of hybridisation properties.

2. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ TP53, PTGS2, FGFR1, PSA, CGA, CYP2D6, ~~and~~ MSMB, and the regulatory regions thereof.

3. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ STMN1, PITX2, PSA, ~~and~~ CGA, and the regulatory regions thereof..

4. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ STMN1, SFN, S100A2, TGFBR2, SYK, GRIN2D, PSA, COX7A2L, VTN, ~~and~~ PRKCD, and the regulatory regions thereof.

5. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ ONECUT2, WBP11, CYP2D6,

DAG1, ERBB2, S100A2, TFF1, TP53, TMEFF2, ESR1, SYK, RASSF1, PITX2, PSAT1, CGA, ~~and~~ PCAF, and the regulatory regions thereof.

6. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ TP53, PTGS2, PITX2, CYP2D6, MSMB, WBP11, TMEFF2, ESR1, PITX2, ERBB2, ~~and~~ PCAF, and the regulatory regions thereof.

7. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ TP53, PTGS2, CYP2D6, ~~and~~ MSMB, and the regulatory regions thereof.

8. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ PITX2, and the regulatory regions thereof.

9. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ WBP11, TMEFF2, ESR1, PITX2, ERBB2, ~~and~~ PCAF, and the regulatory regions thereof.

10. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ STMN1, SFN, TGFBR2, FGFR1, SYK, GRIN2D, PSA, COX7A2L, VTN, PRKCD, ONECUT2, CYP2D6, DAG1, S100A2, TFF1, TP53, SYK, RASSF1, PSAT1, ~~and~~ CGA, and the regulatory regions thereof.

11. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ FGFR1, PSA, ~~and~~ CGA, and the regulatory regions thereof.

12. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ STMN1, PSA, ~~and~~ CGA, and the regulatory regions thereof.

13. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ STMN1, SFN, S100A2, TGFBR2, SYK, GRIN2D, PSA, COX7A2L, VTN, ~~and~~ PRKCD, and the regulatory regions thereof.

14. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein the gene group consists of ~~said genes are selected from the group consisting of~~ ONECUT2, CYP2D6, DAG1, S100A2, TFF1, TP53, SYK, RASSF1, PSAT1, ~~and~~ CGA, and the regulatory regions thereof.

15. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein ~~said~~ the at least one target nucleic acid ~~or acids comprise essentially one or more sequences~~ sequence is selected from the group consisting essentially of SEQ ID NOS: 27, 40, 122, 43, 74, 127, 86, 90, 128, 105, 115, 121, 126, 129, 125, 132, 122, 123, 131, 127, 130, 124, ~~and~~ 128, and sequences complementary thereto.

16. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, ~~said~~ the at least one target nucleic acid ~~or acids comprise essentially one or more sequences~~ sequence is selected from the group consisting essentially of SEQ ID NOS: 68, 50, 74, 90, 91, 92, ~~and~~ 99, and sequences complementary thereto.

17. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein ~~said~~ the at least one target nucleic acid ~~or acids comprise essentially one or more sequences~~ sequence is selected from the group consisting essentially of SEQ ID NOs: 27, 83, 90, ~~and~~ 91, and sequences complementary thereto.

18. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein ~~said~~ the at least one target nucleic acid ~~or acids comprise essentially one or more sequences~~ sequence is selected from the group consisting essentially of SEQ ID NOs: 27, 40, 41, 43, 78, 86, 90, 105, 115, ~~and~~ 121, and sequences complementary thereto.

19. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1, wherein ~~said~~ the at least one target nucleic acid ~~or acids comprise essentially one or more sequences~~ sequence is selected from the group consisting essentially of SEQ ID NOs: 126, 137, 129, 125, 132, 122, 123, 131, 133, 134, 127, 130, 135, 124, 128, ~~and~~ 136, and sequences complementary thereto.

20. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1 ~~Claims 1 to 19~~, wherein said cell proliferative disorder of the breast tissue is selected from the group consisting of ductal carcinoma *in situ*, lobular carcinoma, colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic carcinoma, intraductal carcinoma *in situ*, lobular carcinoma *in situ* and papillary carcinoma *in situ*.

21. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1 ~~Claims 1 to 20~~, wherein said subjects are at least one of estrogen and ~~and/or~~ progesterone receptor positive.

22. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1 ~~Claims 1 to 5 and 10 to 14~~, wherein said therapy is for the treatment of a relapse or metastatic cell proliferative disorder of the breast tissues.

23. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 1 ~~Claims 1 to 9~~, wherein said therapy is an adjuvant treatment.

24. (Currently amended) ~~A~~ The method of ~~according to~~ Claim 23, wherein said subjects did not receive a chemotherapeutic treatment.

25. (Currently amended) A nucleic acid molecule consisting essentially of a sequence at least 18 contiguous bases in length of a sequence selected ~~according to one of the sequences taken~~ from the sequence group consisting of SEQ ID NOS: 299, 300, 325, 326, 327, 328, 331, 332, 345, 346, 381, 382, 393, 394, 401, 402, 411, 412, 417, 418, 425, 426, 427, 428, 429, 430, 443, 444, 455, 456, 475, 476, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 573, 574, 599, 600, 601, 602, 605, 606, 619, 620, 655, 656, 667, 668, 675, 676, 685, 686, 691, 692, 699, 700, 701,

702, 703, 704, 717, 718, 729, 730, 749, 750, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, ~~and~~ 794, and sequences complementary thereto.

26. (Currently amended) ~~A~~ The nucleic acid molecule of Claim 25, wherein the sequence group consists of ~~consisting essentially of a sequence at least 18 bases in length according to one of the sequences taken from the group consisting of~~ SEQ ID NOS: 345, 346, 381, 382, 393, 394, 425, 426, 427, 428, 429, 430, 443, 444, 619, 620, 655, 656, 667, 668, 699, 700, 701, 702, 703, 704, 717, ~~and~~ 718, and sequences complementary thereto.

27. (Currently amended) ~~A~~ The nucleic acid molecule of Claim 25, wherein the sequence group consists of ~~consisting essentially of a sequence at least 18 bases in length according to one of the sequences taken from the group consisting of~~ SEQ ID NOS: 299, 300, 411, 412, 425, 426, 427, 428, 573, 574, 685, 686, 699, 700, 701, ~~and~~ 702, and sequences complementary thereto.

28. (Currently amended) ~~A~~ The nucleic acid molecule of Claim 25, wherein the sequence group consists of ~~consisting essentially of a sequence at least 18 bases in length according to one of the sequences taken from the group consisting of~~ SEQ ID NOS: 299, 300, 325, 326, 327, 328, 331, 332, 401, 402, 417, 418, 425, 426, 455, 456, 475, 476, 487, 488, 573, 574, 599, 600, 601, 602, 605, 606, 675, 676, 691, 692, 699, 700, 729, 730, 749, 750, 761, ~~and~~ 762, and sequences complementary thereto.

29. (Currently amended) ~~A~~ The nucleic acid molecule of Claim 25, wherein the sequence group consists of ~~consisting essentially of a sequence at least 18 bases in length according to one of the sequences taken from the group consisting of~~ SEQ ID NOS: 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, and 794, and sequences complementary thereto.

30. (Currently amended) An oligomer~~, in particular an oligonucleotide or peptide nucleic acid (PNA) oligomer, said oligomer~~ consisting essentially of a ~~at least one base~~ sequence ~~having a length~~ of at least 10 contiguous nucleotides in length which hybridises to or is identical to a sequence selected from the sequence group consisting of ~~one of the nucleic acid sequences according to~~ SEQ ID NO: 299, 300, 325, 326, 327, 328, 331, 332, 345, 346, 381, 382, 393, 394, 401, 402, 411, 412, 417, 418, 425, 426, 427, 428, 429, 430, 443, 444, 455, 456, 475, 476, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 573, 574, 599, 600, 601, 602, 605, 606, 619, 620, 655, 656, 667, 668, 675, 676, 685, 686, 691, 692, 699, 700, 701, 702, 703, 704, 717, 718, 729, 730, 749, 750, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, ~~and~~ 794, and contiguous portions thereof.

31. (Currently amended) The oligomer of Claim 30, wherein the sequence group consists of ~~An oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA) oligomer, said oligomer consisting essentially of at least one base sequence having a length of at least 10 nucleotides which hybridises to or is identical to one of the nucleic acid sequences according to~~ SEQ ID NO: 345, 346, 381, 382, 393, 394, 425, 426, 427, 428, 429, 430, 443, 444, 619, 620, 655, 656, 667, 668, 699, 700, 701, 702, 703, 704, 717, ~~and~~ 718, and contiguous portions thereof.

32. (Currently amended) The oligomer of Claim 30, wherein the sequence group consists of ~~An oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA) oligomer, said oligomer consisting essentially of at least one base sequence having a length of at least 10 nucleotides which hybridises to or is identical to one of the nucleic acid sequences according to~~ SEQ ID NO: 299, 300, 411, 412, 425, 426, 427, 428, 573, 574, 685, 686, 699, 700, 701, ~~and~~ 702, and contiguous portions thereof.

33. (Currently amended) The oligomer of Claim 30, wherein the sequence group consists of ~~An oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA) oligomer, said oligomer consisting essentially of at least one base sequence having a length of at least 10 nucleotides which hybridises to or is identical to one of the nucleic acid sequences according to~~

SEQ ID NO: 299, 300, 325, 326, 327, 328, 331, 332, 401, 402, 417, 418, 425, 426, 455, 456, 475, 476, 487, 488, 573, 574, 599, 600, 601, 602, 605, 606, 675, 676, 691, 692, 699, 700, 729, 730, 749, 750, 761, ~~and~~ 762, and contiguous portions thereof.

34. (Currently amended) The oligomer of Claim 30, wherein the sequence group consists of ~~An oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA) oligomer, said oligomer consisting essentially of at least one base sequence having a length of at least 10 nucleotides which hybridises to or is identical to one of the nucleic acid sequences according to~~ SEQ ID NO: 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, ~~and~~ 794, and contiguous portions thereof.

35. (Currently amended) The oligomer of Claim 30 ~~as recited in any one of Claims 30 to 34~~, wherein the contiguous base sequence includes at least one CpG dinucleotide.

36. (Original) A set of oligomers, comprising at least two oligomers according to any of Claims 30 to 35.

37. (Currently amended) The set of oligomers of Claim 36, wherein ~~A set of oligonucleotides as recited in one of Claims 30 to 36, characterised in that~~ at least one oligomer ~~oligonucleotide~~ is bound to a solid phase.

38. (Currently amended) The set of oligomers of Claim 36, wherein the set is suitable for use ~~A set of at least two oligonucleotides as recited in one of Claims 30 to 36, which is used~~ as primer oligonucleotides for the amplification of a sequence selected from the sequence group consisting of ~~nucleic acid sequences comprising one of~~ SEQ ID NO: 299, 300, 325, 326, 327, 328, 331, 332, 345, 346, 381, 382, 393, 394, 401, 402, 411, 412, 417, 418, 425, 426, 427, 428, 429, 430, 443, 444, 455, 456, 475, 476, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 573, 574, 599, 600, 601, 602, 605, 606, 619, 620, 655, 656, 667, 668, 675, 676, 685, 686, 691, 692,

699, 700, 701, 702, 703, 704, 717, 718, 729, 730, 749, 750, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, ~~and~~ 794, ~~and~~ sequences complementary thereto, and contiguous portions thereof.

39. (Currently amended) A method for determining methylation state or for detecting single nucleotide polymorphisms, comprising using ~~Use of~~ a set of oligonucleotides comprising at least two ~~of the~~ oligomers according to any of Claims 30 to 38 in a suitable assay for detecting ~~the~~ cytosine methylation state or ~~and/or~~ single nucleotide polymorphisms ~~(SNPs)~~ within a sequence selected from the sequence group consisting of ~~the sequences taken from the group~~ SEQ ID NOS: 27, 40, 122, 43, 74, 127, 86, 90, 128, 105, 115, 121, 126, 129, 125, 132, 122, 123, 131, 127, 130, 124, ~~and~~ 128, and sequences complementary thereto.

40. (Currently amended) A method for manufacturing an arrangement of different oligomers (array) fixed to a carrier material and suitable for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising one or more drugs which target the estrogen receptor pathway or are involved in estrogen metabolism, production, or secretion, by analysis of the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of ~~any of the CpG dinucleotides of the group~~ SEQ ID NOS: 27, 40, 122, 43, 74, 127, 86, 90, 128, 105, 115, 121, 126, 129, 125, 132, 122, 123, 131, 127, 130, 124, and 128, comprising coupling ~~wherein~~ at least one oligomer according to any of the Claims 30 to 35 ~~is coupled~~ to a solid phase.

41. (Currently amendedl) An arrangement of different oligomers (array) obtainable according to the method of Claim 40.

42. (Currently amended) The arrangement of Claim 41, wherein the oligomers are at least one of oligonucleotides and ~~An array of different oligonucleotide and/or~~ PNA-oligomer sequences ~~as recited in Claim 41~~, wherein the carrier material is a planar ~~characterised in that said oligonucleotides are arranged on a plane~~ solid phase, and wherein the oligomers are arranged thereon in the form of a rectangular or hexagonal lattice.

43. (Currently amended) The arrangement of Claim 41, wherein the carrier material comprises a material selected from the group consisting of ~~array as recited in any of the Claims 41 or 42, characterised in that the solid phase surface is composed of~~ silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, ~~or~~ gold, and combinations thereof.

44. (Currently amended) An oligomer array suitable ~~A DNA- and/or PNA-array~~ for predicting ~~breast cell proliferative disorders'~~ response of a breast cell proliferative disorder to a therapy involving treatment with ~~comprising~~ one or more drugs that ~~which~~ target the estrogen receptor pathway or that are involved in estrogen metabolism, production~~,~~ or secretion, by analysis of the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of ~~any of the CpG dinucleotides of the group~~ SEQ ID NOS: 27, 40, 122, 43, 74, 127, 86, 90, 128, 105, 115, 121, 126, 129, 125, 132, 122, 123, 131, 127, 130, 124, and 128, the array comprising at least one oligomer ~~nucleic acid~~ according to any of the Claims 30 to 35.

45. (Currently amended) A method for predicting the responsiveness of a subject, with a breast cell proliferative disorder, to a therapy involving treatment with one or more drugs that target the estrogen receptor pathway or that are involved in estrogen metabolism, production or secretion, said method comprising ~~according to any one of Claims 1 to 24 comprising the following steps~~:

a) obtaining, from a subject, a biological sample containing genomic DNA;~~,~~

b) isolating ~~extracting~~ the genomic DNA;~~,~~

c) contacting the isolated genomic DNA, or a portion thereof, with an agent or combination of agents suitable to convert ~~converting~~ cytosine bases ~~in the genomic DNA sample which~~ that are unmethylated at the 5-position~~,~~ to uracil, or to another base which is dissimilar to cytosine in terms of base pairing behaviour, to provide a pretreated DNA;

d) amplifying at least one pretreated DNA sequence ~~fragment~~, or a portion thereof, ~~of the pretreated genomic DNA, wherein said fragments comprise one or more sequences~~ selected from the sequence group consisting of SEQ ID NOS: 299, 300, 325, 326, 327, 328, 331, 332, 345, 346, 381, 382, 393, 394, 401, 402, 411, 412, 417, 418, 425, 426, 427, 428, 429, 430, 443, 444, 455, 456, 475, 476, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 573, 574, 599, 600,

601, 602, 605, 606, 619, 620, 655, 656, 667, 668, 675, 676, 685, 686, 691, 692, 699, 700, 701, 702, 703, 704, 717, 718, 729, 730, 749, 750, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, ~~and~~ 794, ~~and~~ sequences complementary thereto, and contiguous portions thereof; and

e) determining, based on the amplification or on analysis of the nucleic acid amplificate, the methylation status of one or more genomic CpG dinucleotides, whereby responsiveness to the therapy is, at least in part, predicted ~~by analysis of the amplificate nucleic acids~~.

46. (Currently amended) The method of ~~according to~~ Claim 45, wherein the sequence group consists of ~~characterised in that Step d) said fragments comprise one or more sequences selected from the group consisting of~~ SEQ ID NO: 345, 346, 381, 382, 393, 394, 425, 426, 427, 428, 429, 430, 443, 444, 619, 620, 655, 656, 667, 668, 699, 700, 701, 702, 703, 704, 717, ~~and~~ 718, ~~and~~ sequences complementary thereto, and contiguous portions thereof.

47. (Currently amended) The method of ~~according to~~ Claim 45, wherein the sequence group consists of ~~characterised in that Step d) said fragments comprise one or more sequences selected from the group consisting of~~ SEQ ID NO: 299, 300, 411, 412, 425, 426, 427, 428, 573, 574, 685, 686, 699, 700, 701, ~~and~~ 702, ~~and~~ sequences complementary thereto, and contiguous portions thereof.

48. (Currently amended) The method of ~~according to~~ Claim 45, wherein the sequence group consists of ~~characterised in that Step d) said fragments comprise one or more sequences selected from the group consisting of~~ SEQ ID NO: 299, 300, 325, 326, 327, 328, 331, 332, 401, 402, 417, 418, 425, 426, 455, 456, 475, 476, 487, 488, 573, 574, 599, 600, 601, 602, 605, 606, 675, 676, 691, 692, 699, 700, 729, 730, 749, 750, 761, ~~and~~ 762, ~~and~~ sequences complementary thereto, and contiguous portions thereof.

49. (Currently amended) The method of ~~according to~~ Claim 45, wherein the sequence group consists of ~~characterised in that Step d) said fragments comprise one or more sequences selected from the group consisting of~~ SEQ ID NO: 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517,

518, 519, 520, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, ~~and~~ 794, ~~and~~ sequences complementary thereto, and contiguous portions thereof.

50. (Currently amended) The method of ~~according to~~ Claim 45, wherein determining in e) comprises ~~characterised in that Step e) is carried out by means of~~ hybridisation of at least one oligonucleotide selected from the group consisting of SEQ ID NOS:1691-1692, 1733-1736, 1925-1932, 1941-1954, 1965-2141 and SEQ ID NO:2142 ~~according to SEQ ID NO: 1691 to 1692, 1733 to1736, 1925-1932, 1941-1954, and 1965 to 2142~~.

51. (Currently amended) The method of ~~according to~~ Claim 45, wherein determining in e) comprises ~~characterised in that Step e) is carried out by means of~~ hybridisation of at least one oligonucleotide selected from the group consisting of SEQ ID NOS:2011-2012, 2017-2024, 2031-2043, and SEQ ID NO:2044 ~~according to SEQ ID NO: 2011, 2012, 2017 to 2024, 2031 to 2035, 2035, 2036, 2036, 2037, 2037, 2038, and 2038 to 2044~~.

52. (Currently amended) The method of ~~according to~~ Claim 45, wherein determining in e) comprises ~~characterised in that Step e) is carried out by means of~~ hybridisation of at least one oligonucleotide selected from the group consisting of SEQ ID NOS:2003-2029, and SEQ ID NO:2030 ~~according to SEQ ID NO: 2003 to 2030~~.

53. (Currently amended) The method of ~~according to~~ Claim 45, wherein determining in e) comprises ~~characterised in that Step e) is carried out by means of~~ hybridisation of at least one oligonucleotide selected from the group consisting of SEQ ID NOS:2003-2020, 2045-2111, and SEQ ID NO:2112 ~~according to SEQ ID NO: 2003 to 2020 and 2045 to 2112~~.

54. (Currently amended) The method of ~~according to~~ Claim 45, wherein determining in e) comprises ~~characterised in that Step e) is carried out by means of~~ hybridisation of at least one oligonucleotide selected from the group consisting of SEQ ID NOS:1691-1692, 1733-1736, 1925-1932, 1941-1954, 1965-2002, 2011-2025, 2045-2052, 2069-2078, 2127-2133, and SEQ ID

NO:2134 ~~according to SEQ ID NO: 1691 to 1692, 1733 to 1736, 1925 to 1932, 1941 to 1954, 1965 to 2002, 2011 to 2025, 2045 to 2052, 2069 to 2078 and 2127 to 2134~~.

55. (Currently amended) The method of ~~as recited in~~ Claim 45, wherein determining in e) comprises ~~characterised in that Step e) is carried out by means of~~ hybridisation of at least one oligonucleotide according to any of Claims 30 to 35 ~~17 to 21~~.

56. (Currently amended) The method of ~~as recited in~~ Claim 45, wherein determining in e) comprises ~~characterised in that Step e) is carried out by means of~~ hybridisation of at least one oligonucleotide according to any of Claims 30 to 35, ~~17 to 21~~ and extension of the at least one ~~said~~ hybridised oligonucleotide(s) by ~~means of~~ at least one nucleotide base.

57. (Currently amended) The method of ~~as recited in~~ Claim 45, wherein determining in e) comprises ~~characterised in that Step e) is carried out by means of~~ sequencing.

58. (Currently amended) The method of ~~as recited in~~ Claim 45, wherein amplifying in d) comprises ~~characterised in that Step d) is carried out~~ using methylation-specific ~~methylation-specific~~ primers.

59. (Currently amended) The method of ~~as recited in~~ Claim 45, further comprising in ~~step~~ d) ~~the~~ use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOS: 299, 300, 325, 326, 327, 328, 331, 332, 345, 346, 381, 382, 393, 394, 401, 402, 411, 412, 417, 418, 425, 426, 427, 428, 429, 430, 443, 444, 455, 456, 475, 476, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 573, 574, 599, 600, 601, 602, 605, 606, 619, 620, 655, 656, 667, 668, 675, 676, 685, 686, 691, 692, 699, 700, 701, 702, 703, 704, 717, 718, 729, 730, 749, 750, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, ~~and~~ 794, and

complements thereof, wherein said at least one nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of a ~~the~~ nucleic acid to which it is hybridized.

60. (Currently amended) The method of ~~as recited in~~ Claim 45, wherein determining in e) comprises use ~~characterised in that Step e) is carried out by means of a combination~~ of at least two of the methods described in any one of Claims 55-57 ~~38 to 42~~.

61. (Currently amended) The method of ~~as recited in~~ Claim 45, wherein contacting in c) is with an agent, or combination of agents, comprising ~~characterised in that the treatment is carried out by means of a solution of a~~ bisulfite, hydrogen sulfite or disulfite.

62. (Currently amended) A method for predicting the responsiveness of a subject, with a breast cell proliferative disorder, to a therapy involving treatment with one or more drugs that target the estrogen receptor pathway or that are involved in estrogen metabolism, production or secretion, said method comprising ~~according to any one of Claims 1 to 24 comprising the following steps~~:

a) obtaining, from a subject, a biological sample containing genomic DNA;~~,~~

b) isolating ~~extracting~~ the genomic DNA;~~,~~

c) digesting the isolated genomic DNA, or a portion thereof, comprising at least one ~~or more of the sequences~~ sequence selected from the sequence group consisting of SEQ ID NOS:27, 40, 41, 43, 50, 68, 74, 78, 83, 86, 90-92, 99, 105, 115, 121-137 ~~SEQ ID NOS 27, 40, 122, 43, 74, 127, 86, 90, 128, 105, 115, 121, 126, 129, 125, 132, 122, 123, 131, 127, 130, 124, and 128~~, and sequences complementary thereto, with one or more methylation-sensitive ~~methylation-sensitive~~ restriction enzymes;~~,~~ and

d) determining ~~of~~ the DNA fragments generated in ~~the digest of step c)~~, whereby responsiveness to the therapy is, at least in part, predicted.

63. (Currently amended) The method of ~~according to~~ Claim 62, wherein the sequence group consists of ~~characterised in that the target sequence or sequences digested in Step c) comprises one or more sequences from the group consisting of~~ SEQ ID NOS:50, 68, ~~SEQ ID NOs 68, 50,~~ 74, 90, 91, 92, ~~and~~ 99, and sequences complementary thereto.

64. (Currently amended) The method of ~~according to~~ Claim 62, wherein the sequence group consists of ~~characterised in that the target sequence or sequences digested in Step c) comprises one or more sequences from the group consisting of~~ SEQ ID NOS:~~SEQ ID NOs~~ 27, 83, 90, and 91, ~~and~~ sequences complementary thereto.

65. (Currently amended) The method of ~~according to~~ Claim 62, wherein the sequence group consists of ~~characterised in that the target sequence or sequences digested in Step c) comprises one or more sequences from the group consisting of~~ SEQ ID NOS:~~SEQ ID NOs~~ 27, 40, 41, 43, 78, 86, 90, 105, 115, ~~and~~ 121, and sequences complementary thereto.

66. (Currently amended) The method of ~~according to~~ Claim 62, wherein the sequence group consists of ~~characterised in that the target sequence or sequences digested in Step c) comprises one or more sequences from the group consisting of~~ SEQ ID NOS:~~SEQ ID NOs~~ 126, 137, 129, 125, 132, 122, 123, 131, 133, 134, 127, 130, 135, 124, 128, and 136.

67. (Currently amended) The ~~A~~ method of Claim 62, further comprising, prior to d), amplifiying ~~according to any one of Claims 62 to 66, wherein~~ the DNA digest ~~is amplified prior to step d)~~.

68. (Currently amended) The method of any ~~as recited in~~ one of Claims 45 ~~to 54~~ and 67, wherein ~~characterised in that~~ more than six different fragments having a length of 100 - 200 base pairs are amplified.

69. (Currently amended) The method of any ~~as recited in~~ one of Claims 45 and 67, wherein ~~to 54 and 68 characterised in that the~~ amplification of several DNA segments is carried out in one reaction vessel.

70. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 45 and 67, wherein amplifying is by means of ~~to 54 and 68, characterised in that the polymerase is~~ a heat-resistant DNA polymerase.

71. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 45 and 67, wherein amplifying is by means of a ~~to 54 and 70, characterised in that the amplification is carried out by means of the~~ polymerase chain reaction (PCR).

72. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 45 and 67, wherein ~~to 54 and 69 to 70, characterised in that~~ the amplificates carry detectable labels.

73. (Currently amended) The method of ~~according to~~ Claim 72, wherein said labels are selected from the group consisting of fluorescence labels, radionuclides, ~~and/or~~ detachable molecule fragments having a typical mass which can be detected in a mass spectrometer, and combinations thereof.

74. (Currently amended) The method of Claim 73, wherein ~~as recited in one of the Claims 45 and 67 to 54 and 69 to 73, characterised in that the~~ amplificates or fragments of the amplificates are detected in the mass spectrometer.

75. (Currently amended) The method of Claim 74, wherein ~~as recited in one of the Claims 74 and/or 73, characterised in that the~~ produced fragments have a single positive or negative net charge for better detectability in the mass spectrometer.

76. (Currently amended) The method of Claim 74, wherein ~~as recited in one of Claims 73 to 75, characterised in that~~ detection is carried out and visualised by means of at least one of matrix assisted laser desorption/ionisation mass spectrometry (MALDI), and ~~or using~~ electron spray mass spectrometry (ESI).

77. (Currently amended) The method of any ~~as recited in~~ one of ~~the~~ Claims 45 and 62, wherein ~~to 76, characterised in that~~ the biological sample containing genomic DNA is obtained from a source selected from the group consisting of cells or cellular components which contain DNA, ~~sources of DNA comprising, for example,~~ cell lines, histological slides, biopsies, tissue embedded in paraffin, breast tissues, blood, plasma, lymphatic fluid, lymphatic tissue, duct cells, ductal lavage fluid, nipple aspiration fluid, bone marrow, and combinations thereof.

78. (Currently amended) A kit, comprising a reagent having at least one of bisulfite, disulfite, and hydrogen sulfite, ~~bisulfite (= disulfite, hydrogen sulfite) reagent~~ as well as oligonucleotides and/or PNA-oligomers according to any one of Claims 30 to 38.

79. (Currently amended) The ~~A~~ kit of ~~according to~~ Claim 78, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethyLight~~Methyl light~~, HeavyMethyl~~Heavy Methyl~~, nucleic acid sequencing, and combinations thereof.

80. (Cancelled) ~~The use of a method according to one of Claims 1 to 24, 45 to 77, a nucleic acid according to Claims 25 to 29, of an oligonucleotide or PNA-oligomer according to one of the Claims 30 to 35, of a kit according to Claim 78 or 79, of an array according to one of the Claims 40 to 44, a method of manufacturing an array according to Claim 39 or of a set of oligonucleotides according to one of Claims 36 to 38 for the treatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders.~~